AMENDMENTS TO THE SPECIFICATION

Please amend paragraph [00110] as follows:

For many applications, it is desirable to preferentially enrich mRNA with respect to other cellular RNAs, such as transfer RNA (tRNA) and ribosomal RNA (rRNA). Most mRNAs contain a poly(A) tail at their 3' end. This allows them to be enriched by affinity chromatography, for example, using oligo(dT) or poly(U) coupled to a solid support, such as cellulose or ~~Sephadex™~~ SEPHADEX® (see Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, vol. 2, Current Protocols Publishing, New York (1994)). Once bound, poly(A)+ mRNA is eluted from the affinity column using 2 mM EDTA/0.1% SDS.

Please amend paragraph [00142] as follows:

The methods of the invention preferably use a control or reference sample, which can be any suitable sample against which changes in cellular constituents can be determined. In one embodiment, the control or reference sample is generated by pooling together the plurality of cellular constituents, e.g., a plurality of transcripts or cDNAs, or a plurality of protein species, from a plurality of breast cancer patients. Alternatively, the control or reference sample can be generated by pooling together purified or synthesized cellular constituents, e.g., a plurality of purified or synthesized transcripts or cDNAs, a plurality of purified or synthesized protein species. In one embodiment, synthetic RNAs for each transcripts or cDNAs are pooled to form the control or reference sample. Preferably, the abundances of synthetic RNAs are approximately the abundances of the corresponding transcripts in a real tumor pool. The differential expression of marker genes for each individual patient sample is measured against this control sample. In one embodiment, 60-mer oligonucleotides corresponding to the probe sequences on a microarray used to assay the expression levels of the diagnostic/prognostic

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